

# SEQUENCE LISTING

<110> Duvick, Jonathan P.  
Gilliam, Jacob T.  
Maddox, Joyce R.  
Rao, Aravinda Gururaj  
Crasta, Oswald R.  
Folkerts, Otto

<120> Amino Polyl Amine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

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<141> 2000-09-05

<151> US 09'192,886

<151> 1998-07-29

<161> US 09'134,891

<161> 1998-08-21

<166> US 09'382,159

<166> 1998-07-14

<166> US 09'382,163

<166> 1998-07-12

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<170> PatentIn version 3.1

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attgtcgatc gacgtcgatg ctggatatct tggcaaatga gatggggcca cagctcgatt 180

ggaggacgcc cgagaagcct tgttcggccc aaccaggcct gtcccatacg aagactatct 240

tgctatagta ggcacaggata gaattttccg ccaatgcttg ctctcggggg ggaagaggtg 300

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<210> 4  
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
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gag gag atg gat cgt gta ggg gga aag act ctg agc gta caa tgg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc gcc agg aag act atc aac gac ctc ggc gct ggg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga tgg ttr gaa aga tit cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg aag act gga aat tcc atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt ggc gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag ggc aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc gcc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tgg gac aag aaa gac gcc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat atg cga tgc aaa aca ggt atg cag tgg att tgc cat gcc atg	672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
210 215 220	
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Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
225 230 235 240	
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Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
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Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu	
260 265 270	
tat ccc acc ttg aca ttt tta cca cct ctt ccc gcc gag aag caa gca	964
Tyr Pro Phe Ser Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
275 280 285	
ttg gcc gaa aat tct atc ctg gcc tcc tat agc aag ata gtc ttc gta	917
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
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tcg gac aag ccg tcg tcg gcc gaa caa gcc ttc tcg gcc gtc ctc caa	960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
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tcg agc tct gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tcg tcc att acc tgt ttc atg gtc gga gac ccg gga ccg	1056
Asp Arg Glu Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
340 345 350	
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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
355 360 365	
caa ctc ccg gca gcc tcc gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Gln Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tcg tcg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
385 390 395 400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
405 410 415	
ggc ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr	
420 425 430	
tct tta gtt tcg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa	1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
435 440 445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1389
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
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4211 · 462  
 4212 · PRT  
 4213 · *Exophiala spinifera*

4400 · 6

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
 85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
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Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
 115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
 130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
 165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
 180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205

Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
 210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
 225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
 245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
 260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
 275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
 290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
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 325 330 335

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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
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Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
 370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
 385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
 405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
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01130  
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 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45  
 ccc gcc agg aag act atc aac gac ctc ggc gct ggc tgg atc aat gac 192  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60  
 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
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 85 90 95  
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Val Ala Ser Ala Leu Ala Gln Leu Leu Pro Val Trp Ser Gln Leu Ile	
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Gln Gln His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Gln Lys Gln Leu Asn Leu	
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
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gtg gaa gcc cac gag atc agc atg ctt ttt ctc aac gac tac atc aac	576
Val Gln Ala His Gln Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tgg gac aag aaa gac gcc gcc	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
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Gln Tyr Val Arg Cys Lys Thr	
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Gly Met Gln Ser Ile Cys His Ala Met Ser	
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230 235 240	
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Ile Gln Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tgg tta cgg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
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Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Gln Lys Gln Ala Leu	
275 280 285	
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Ala Gln Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
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Asp Lys Pro Trp Trp Arg Gln Gln Gly Phe Ser Gly Val Leu Gln Ser	
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Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp  
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 340 345 350  
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 370 375 380 385  
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 420 425 430  
 tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcc ggt caa cga 1400  
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 <213> Exophiala spinifera

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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
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Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
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Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
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Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
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Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
 325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
 355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
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Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
 405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
 420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
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 0212 PRT  
 0213 Exophiala spinifera

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25

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
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Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
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Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
 115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
 165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
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Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly  
 210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met  
 225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro  
 245 250 255



Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro  
 260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln  
 275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys  
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His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr  
 305 310 315 320

Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn  
 325 330 335

Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser  
 340 345 350

Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly  
 355 360 365

Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr  
 370 375 380

Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg  
 385 390 395 400

Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu  
 405 410 415

Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg  
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ttg	gag	aag	gca	agg	aaa	gtc	cag	gac	ggc	ggc	ctg	tcg	tgc	ctc	gtt	96
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
		20						25					30			

ctt	gag	ggc	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agg	gta	caa	tgg	144
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
		35				40					45					

ggt	ccc	ggc	agg	aag	act	atc	aac	gac	ctc	ggc	gct	ggg	tgg	atc	aat	192
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55				60						

gac	agg	aac	caa	agg	gaa	gta	tcg	aga	tig	ttt	gaa	aga	ttc	cat	ttg	240
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
65				70					75					80		

gag	ggc	gag	ctc	cag	agg	aag	act	gga	aat	tca	atc	cat	caa	gca	caa	288
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
			85					90					95			

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Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
		100					105					110				

gag	gtt	gca	agt	gca	ctt	gag	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	
	115						120					125				

atc	gaa	gag	cat	agg	ctt	caa	gac	ctc	aag	ggc	agg	cct	cag	ggc	aag	432
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	
	130					135				140						

cgg	ctc	gac	agt	gtg	agg	ttc	gag	cac	tac	tgt	gag	aag	gaa	cta	aac	480
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	
145				150					155					160		

ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	528
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	
			165					170						175		

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
130 135 190	
aag agt gcc acc ggt atc agt aat att ttc tgg gac aag ana gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 215	
ggg cag tat atg cga tgc aaa asa ggt atg cag tgg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac aac ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tgg gca tcc ggc tgt aca gta cga tgg gcc tgg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgg tta cgg acc acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Gln Lys Gln	
275 280 285	
gca ttg gcc gaa aat tat atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccc tgg tgg cgc gaa caa ggc ttc tgg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tgg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
ccg aag tgg tcc caa cag tcc aag cag gta cga caa aag tat gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc caa gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1243  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415

tcc ggc ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcc ggt 1344  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

cga cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

0210: 11

0211: 463

0212: PERT

0213: *Exophiala spinifera*

0220:

0221: misc\_feature

0222: (1)..(3)

0223: Extra lysine in K:trAPAO

0400: 11

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
 165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
 180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
 195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
 210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
 225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
 245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
 260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 305 310 315 320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
 325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly

340

345

350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

&lt;210&gt; 12

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Primer for cloning into vectors N23256 (*Exophiala spinifera*)

&lt;400&gt; 12

ggggaattca aagacaacgt tgcggacgtg gtag

34

&lt;210&gt; 13

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Primer for cloning into vectors N23256 (*Exophiala spinifera*)

&lt;400&gt; 13

ggggggggcgc cctatgctgc tggcaccagg ctac

34

&lt;210&gt; 14

&lt;211&gt; 29

<212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Designed oligo for 3' RACE, N21965 (Exophiala spinifera)

<400> 11  
 tgggttgggtt accgacaacc ttgtatccc 29

<212> 15  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Designed oligo for 5' RACE, N21969 (Exophiala spinifera)

<400> 15  
 tgggttggttc cagacagact ttgtgctg 28

<212> 18  
 <211> 1073  
 <212> DNA  
 <213> Exophiala spinifera

<220>  
 <221> sig\_peptide  
 <222> (1)..(267)  
 <223> yeast alpha mating factor secretion signal

<212>  
 <221> CDS  
 <222> (1)..(1662)  
 <223>

<400> 16  
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48  
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
 1 5 10 15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96  
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
 20 25 30

att cgg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144  
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
 35 40 45

gat att gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192  
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
 50 55 60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240  
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val

65	70	75	80	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gag				288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	95	90	95	
gac gtg gta gag gtg ggt gct ggc ttg agc ggt ttg gaa acg gca cgc				336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Gln Thr Ala Arg	100	105	110	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat				384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Gln Ala Met Asp	115	120	125	
ggt gta ggg gga aag act ctg agt gta caa tgg ggt ccc gcc agg acg				432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	130	135	140	
act atc aac gac ctc gcc gct gcc tgg atc aat gac agc aac caa agc				480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	145	150	155	160
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag gcc gag ctc cag				528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Gln Leu Gln	165	170	175	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act				576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	180	185	190	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca				624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Gln Val Ala Ser Ala	195	200	205	
ctt gog gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc				672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Gln His Ser	210	215	220	
ctt caa gac ctc aag gog agc cct cag gog aag cgg ctc gag agt gtg				720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	225	230	235	240
agc ttc gog cac tac tgt gag aac gaa cta aac ttg cct gct gtt ctc				768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	245	250	255	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac				816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	260	265	270	
gag atc agc atg ctt ttt ctc acc gag tac atc aag agt gcc acc ggt				864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	275	280	285	
ctc agt aat att ttc tgg gac aag aaa gac gcc ggg cag tat atg cga				912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	290	295	300	



tgc aaa aca ggt atg cag tgc att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 305 310 315 320	960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln 325 330 335	1008
tgc gca tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg 340 345 350	1056
agc aaa aag gtc gtg gtt tgc tta cgg aca acc ttg tat ccc acc ttg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu 355 360 365	1104
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn 370 375 380	1152
tct atc ctc ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro 385 390 395 400	1200
tgg tgg cgc gaa caa gcc ttc tgc ggc gtc ctc caa tgc agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp 405 410 415	1248
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp 420 425 430	1296
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln 435 440 445	1344
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala 450 455 460	1392
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu 465 470 475 480	1440
gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala 485 490 495	1488
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc ggc ctc aga acg Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr 500 505 510	1536
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp 515 520 525	1584

aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga ggt gct gca 1632  
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
 530 535 540

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673  
 Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 545 550

0110: 17  
 0111: 554  
 0112: PRT  
 0113: Exophiala spinifera

0400: 17

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
 1 5 10 15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
 20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
 35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
 50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
 65 70 75 80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
 85 90 95

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
 100 105 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
 115 120 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
 130 135 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
 145 150 155 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln

165

170

175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
 180 135 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
 195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser  
 210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val  
 225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
 245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
 260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
 275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg  
 290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
 305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln  
 325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg  
 340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu  
 355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn  
 370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro  
 385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp  
 405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp  
 420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln  
 435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala  
 450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu  
 465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala  
 485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr  
 500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp  
 515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
 530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 545 550

<210> 18  
 <211> 2079  
 <212> DNA  
 <213> Unknown

<220>  
 <223> GST:K:trAPAO 2079 for bacterial expression (Exophiala spinifera)

<220>  
 <221> CDS  
 <222> (1)..(2076)  
 <223>

<220>  
 <221> misc\_feature

02220 (1)..(687)  
 02230 gst fusion + polylinker

02200  
 02210 misc\_feature  
 02220 (688)..(2076)  
 02230 K:trAPAO

02200  
 02210 misc\_feature  
 02220 (688)..(690)  
 02230 Extra lysine

04000 18  
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 gga gcg gtt ttg gat att aga tac ggt gtt tog aga att gca tat agt 336  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	523
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa ctt att gaa ggt atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa ttc agc aag tat ata gca tgg ctt ttg cag ggc tgg cca gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tgg gat ctg gtt cgg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc cgg gaa ttc aaa gac aac gtt ggg gac gtg gta gtg gtg ggc	720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
gct ggc ttg agc ggt ttg gag acg gca cgt aaa gtc cag gcc gcc ggt	768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
ctg tcc tgc ctc gtt ctt gag gcc atg gat cgt gta ggg gga aag act	816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
ctg agc gta caa tgg ggt ccc ggc agg acg act atc aac gac ctc gcc	864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gac ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc gcc gta gca aac cag atc	1200

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tgc	1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tgc att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg ggc gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa gcc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgc aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	

610	615	620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat			1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
625	630	635	640
ctc atc aca ctg ggt tgg ggc ctc aga acg ccg ttc aag agt gtt cat			1958
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
645	650		655
ctc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
660	665		670
gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
675	680		685
gtg cca gca gca tag			2079
Val Pro Ala Ala			
690			

<210> 19  
 <211> 692  
 <212> PRT  
 <213> Unknown

<220>  
 <223> GST:K:trAPAO 2079 for bacterial expression (Exophiala spinifera)

<220>  
 <221> misc\_feature  
 <222> (1)..(687)  
 <223> gst fusion + polylinker

<220>  
 <221> misc\_feature  
 <222> (688)..(2076)  
 <223> K:trAPAO

<220>  
 <221> misc\_feature  
 <222> (688)..(690)  
 <223> Extra lysine

<400> 19

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
		20					25						30		

Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



35

40

45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220

Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
 225 230 235 240

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
 245 250 255

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
 260 265 270

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
275 280 285

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
290 295 300

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
305 310 315 320

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp  
325 330 335

Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
340 345 350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
 500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
 515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
 530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
 545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
 565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
 580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
 595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
 610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
 625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
 645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
 675 680 685

Val Pro Ala Ala  
 690

<210> 20  
 <211> 1464  
 <212> DNA  
 <213> Unknown

4220+  
 4221+ F:trAPA0 fusion with barley alpha amylase (Exophiala spinifera)

4222+  
 4223+ sig\_peptide  
 4224+ (1)..(72)  
 4225+ Barley alpha amylase signal sequence

4226+  
 4227+ misc\_feature  
 4228+ (73)..(1464)  
 4229+ F:trAPA0 cDNA

4230+  
 4231+ CDS  
 4232+ (1)..(1461)  
 4233+

4234+  
 4235+ misc\_feature  
 4236+ (73)..(75)  
 4237+ Added lysine residue

4400+ 20  
 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48  
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 1 5 10 15  
 ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
 20 25 30  
 gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144  
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
 35 40 45  
 gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg 192  
 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
 50 55 60  
 gga aag act ctg agc gta caa tgg ggt ccc ggc agg acg act atc aac 240  
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
 65 70 75 80  
 gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc 288  
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
 85 90 95  
 aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act 336  
 Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
 100 105 110  
 gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct 384

Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro		
	115						120						125				
tat	ggt	gac	tcg	ttg	ctg	agg	gag	gag	gtt	gca	agt	gca	ott	ggg	gaa	432	
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu		
	130					135				140							
ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agg	ott	caa	gac	430	
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp		
	145				150					155				160			
ctc	aag	ggg	agg	ccc	cag	ggg	aag	egg	ctc	gac	agt	gtg	agg	ttc	ggg	528	
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala		
			165						170					175			
cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	ccc	gct	gtt	ctc	ggc	gta	gca	576	
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala		
			180					185						190			
aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	ggc	cac	gag	atc	agg	624	
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser		
	195					200						205					
atg	ctt	ttc	ctc	acc	gac	tac	atc	aag	agt	ggc	acc	ggt	ctc	agt	aat	672	
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn		
	210					215					220						
att	ttc	tgg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	720	
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr		
	225				230				235					240			
ggt	atg	cag	tgg	att	tgc	cat	ggc	atg	tca	aag	gaa	ott	gtt	cca	ggc	768	
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly		
			245					250					255				
tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tgg	gca	tcg	816	
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser		
			260					265					270				
ggc	tgt	aca	gta	cga	tgg	ggc	tgg	ggc	ggc	gtg	ttc	cga	agg	aaa	aag	864	
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys		
		275				280						285					
gtg	gtg	gtt	tgg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	912	
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser		
	290				295					300							
cca	ctt	ctt	ccc	ggc	gag	aag	caa	gca	ttg	ggg	gaa	aat	tct	atc	ctg	960	
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu		
	305			310					315					320			
ggc	tac	tat	agg	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	1008	
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg		
			325					330					335				
gaa	caa	ggc	ttc	tgg	ggc	gtc	ctc	caa	tgg	agg	tgt	gac	ccc	atc	tca	1056	
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser		

340	345	350	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc			1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr			
355	360	365	
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag			1152
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
370	375	380	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag			1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Gln			
385	390	395	400
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag			1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Gln Ile Gln			
405	410	415	
tgg tgg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg			1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
420	425	430	
ccg aac gat ctc atc aca ctg ggt tgg gcg ctc aga aag ccg ttc aag			1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
435	440	445	
agt gtt cat ttc gtt gga aag gag aag tct tta gtt tgg aaa ggg tat			1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
450	455	460	
atg gaa ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg			1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
465	470	475	480
gct agc ctg gtg cca gca gca tag			1464
Ala Ser Leu Val Pro Ala Ala			
485			

<210> 21  
 <211> 487  
 <212> PRT  
 <213> Unknown

<220>  
 <223> K:trAPAO fusion with barley alpha amylase (Exophiala spinifera)

<210>  
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 <222> (73)..(1464)  
 <223> K:trAPAO cDNA

<220>  
 <221> misc\_feature  
 <222> (73)..(75)  
 <223> Added lysine residue

<400> 21

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
20 25 30

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
35 40 45

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
50 55 60

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
65 70 75 80

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
85 90 95

Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
100 105 110

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro  
115 120 125

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
130 135 140

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
145 150 155 160

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys  
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser  
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu  
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg  
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser  
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr  
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys  
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu  
385 390 395 400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu  
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly  
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys  
435 440 445



Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr  
 450 455 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val  
 465 470 475 480

Ala Ser Leu Val Pro Ala Ala  
 485

<210> 22  
 <211> 1803  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
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 <223>

<400> 21  
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 1 5 10 15  
 gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96  
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30  
 aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
 35 40 45  
 gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc 192  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60  
 ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac 240  
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
 65 70 75 80  
 tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg 288  
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95  
 ctg aag gct acc ttt gcc att gac agg ctc cct cct tgc acg ctg gtg 336  
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110  
 cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc 384  
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
 115 120 125  
 acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg 432  
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val

130	135	140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 145 150 155 160			430
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 165 170 175			523
ggg gga aag act ctg agc gta caa tgc ggt ccc gcc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 180 185 190			576
aac gac ctc gcc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205			624
tcc aga ttg ttt gaa aga ttt cat ttg gag agc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220			672
act gga aat tca atc cat caa gca caa gac agt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 225 230 235 240			720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcc Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255			768
gaa ctc ctc ccc gta tgg tcc cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270			816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285			864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc gcc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300			912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320			960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335			1008
aat att ttc tgc gac aag aaa gac gcc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350			1056
aca ggt atg cag tgc att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365			1104

ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tgg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380	1152
tcc ggc tgt aca gta cga tgg gcc tgg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400	1200
aag gtg gtg gtt tgg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415	1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430	1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tgg ggc gtc ctc caa tgg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
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ggg ctg aac gat ctc atc aca ctg ggt tgg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
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1803

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
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Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile

180

185

190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
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Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
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385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
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Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

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500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

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Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
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+2112+ (173)..(1575)
+2113+ espl mat

+2200+
+2211+ misc_feature
+2212+ (1576)..(1611)
+2213+ spacer sequence

+2220+
+2211+ misc_feature
+2212+ (1612)..(3000)
+2213+ K:trAPA0

+2230+
+2211+ CDS
+2212+ (1)..(3000)
+2213+

+2233+
+2211+ misc_feature
+2212+ (1612)..(1614)
+2213+ extra lysine

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Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
65          70          75          80

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Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
85          90          95

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Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly

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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
820 825 830	
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
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Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
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Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
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Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
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Val Ala Ser Leu Val Pro Ala Ala	
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0311 1000  
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 0313 unknown

0320  
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 0339 spacer sequence

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Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
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Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly  
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Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
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340

345

350

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Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala  
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Gln Ala Met Asp Arg Val  
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
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Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
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Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
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Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
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Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
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Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
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Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
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atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc      48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
          -20                      -15                      -10

ctc tcc gcc tcc ctc gcc agc ggc aag gat ttt ccg gtc cgc agg acc      96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
          -5                      -1 1                      5

gat ctg gcc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc      144
Asp Leu Gly Gln Val Gln Leu Ala Gly Asp Val Met Ser Phe Arg
          10                      15                      20

gga ata ccc tat gca gag ccc ccc gtg ggc ggg ctg cgt tgg aag ccg      192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
          25                      30                      35                      40

ccc caa cac gcc cgg ccc tgg gag ggc gtt cgc ccc gcc acc caa ttt      240
  
```

Pro	Gln	His	Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	
			45						50					55		
ggc	tcc	gac	tgc	ttc	ggc	ggc	goc	tac	ctt	cgc	aaa	ggc	agc	ctc	goc	288
Gly	Ser	Asp	Lys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	
			60					65					70			
ccc	ggc	gtg	agg	gag	gac	tgt	ctt	tac	ctc	aac	gta	tgg	ggc	cgc	tca	336
Pro	Gly	Val	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	
		75				90						85				
ggc	gct	aaa	ccc	ggc	cag	tac	ccc	gtc	atg	gtc	tgg	gtc	tac	ggc	ggc	384
Gly	Ala	Lys	Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	
	90					95					100					
ggc	ttc	gct	ggc	ggc	acc	ggc	ggc	atg	ccc	tac	tac	gac	ggc	gag	ggc	432
Gly	Phe	Ala	Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala	
	105				110					115					120	
ctt	ggc	cga	cag	ggc	gtc	gtc	gtg	gtg	acc	ttt	aac	tat	cgc	acc	aac	480
Leu	Ala	Arg	Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn	
			125						130					135		
atc	ctg	ggc	ttt	ttc	gct	cat	ccg	ggt	ctc	tgc	cgc	gag	agg	ccc	acc	528
Ile	Leu	Gly	Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	
		140						145					150			
gga	act	tgc	ggc	aac	tac	ggc	cta	ctc	gac	att	ctc	goc	gat	ctt	cgc	576
Gly	Thr	Ser	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	
	155					160						165				
tgc	gtg	cag	agg	aac	ggc	cgc	ggc	ttc	gga	ggg	gac	ccc	ggc	cga	gtg	624
Trp	Val	Gln	Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	
	170					175					180					
acc	gtc	ttt	ggt	gaa	tgc	ggc	gga	ggc	agg	atc	gga	ctt	ctg	ctc		672
Thr	Val	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	
	185				190				195					200		
acc	tgc	cgc	ctg	agg	cga	ccg	ctc	ggc	acc	ctc	ggc	gac	agg	ggc	tgc	720
Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	
			205					210					215			
cca	ggg	ctg	acc	cga	ccg	ctc	ggc	acc	ctc	ggc	gac	agg	ggc	ggc	tgc	768
Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	
			220					225				230				
ggc	gag	cgc	ctc	gac	ggc	gat	ctt	tgc	cga	ctg	cgc	tgc	acc	gac	cca	816
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	
	235					240						245				
ggc	acc	ctg	atg	ggc	cgc	ggc	gac	ggc	ggc	cgc	ccg	gca	tgc	cgc	gac	864
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	
	250					255					260					
ctg	cgc	agg	ccg	cgt	ccg	acc	gga	ccg	atc	gtc	gat	ggc	cat	gtg	ctg	912
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	

265	270	275	280	
cag cag acc gac agc gag gag atc gag gag gga cag ctg gag cag gtt				960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val				
	285	290	295	
gag gtc ctg atc gga acc aat ggc gac gaa gga cgc gcc ttc ctg ggg				1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Gln Gly Arg Ala Phe Leu Gly				
	300	305	310	
gag gag cag atg gag acg cca gag gar tac caa gcc tat ctg gag cgc				1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Gln Ala				
	315	320	325	
cag ttt gag gac caa gcc gcc gcc gtc gag gcc tgc tat cca ctg gac				1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp				
	330	335	340	
gga cgg gcc acc cca aag gaa atg gtc gag cgc atc ttc gga gac aat				1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn				
	345	350	355	360
cag ttc aat cgg gga gtc tgc gcc ttc tgc gag gag ctg gtc cgc cag				1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Gln Ala Leu Val Arg Gln				
	365	370	375	
gga gag ccc ctg tga cgt tat cag ttc aac ggc aat acc gag ggt gga				1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Gln Gly Gly				
	380	385	390	
aga gag cag gct acc cac gga gcc gaa att ccc tac gtt ttc gga gtc				1296
Arg Ala Pro Ala Thr His Gly Ala Gln Ile Pro Tyr Val Phe Gly Val				
	395	400	405	
ttc aag ctg gac gag ttc ggt ctg ttc gat tgg cgc ccc gag gga ccc				1344
Phe Lys Leu Asp Glu Leu Phe Asp Trp Pro Pro Glu Gly Pro				
	410	415	420	
acg ccc gcc gac cgt gag ctg ggc caa ctg atg tcc tcc gcc tgg gtc				1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val				
	425	430	435	440
cgg ttc gcc aag aat ggc gac ccc gcc gga gag gcc ctg acc tgg cct				1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro				
	445	450	455	
gcc tat tct acg ggc aag tgc acc atg aca ttc ggt ccc gag ggc cgc				1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg				
	460	465	470	
gag gag gtc gtc tgc ccc gga cct tcc atc ccc cct tgc gag gat ggc				1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly				
	475	480	485	
gcc aag gag gga ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc				1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser				
	490	495	500	

aaa gac aac gtt ggc gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
505 510 515 520	
ttg gag acg gaa cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag ggc atg gat ggt gta ggg gga aag act ctg agc gta caa tgg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcc tgg atc aat	1776
Gly Pro Gly Arg Phe Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag gcc gag ctc cag agg acg act gga aat tca atc cat caa gaa caa	1872
Glu Gly Glu Leu Gln Arg Thr Phe Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
gac ggt aca acc act aca gct cat cat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
605 610 615	
gag gtt gaa agt gaa ctt ggc gaa ctc ctc ccc gta tgg tct cag ctg	1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
620 625 630	
atc gaa gag cat agc ctt caa gac ctc aag gcc agc cct cag gcc aag	2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
635 640 645	
cgg ctc gac agt gtg agc ttc gcc caa tac tgt gag aag gaa cta aac	2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
650 655 660	
ttg cct gct gtt ctc ggc gta gaa aac cag atc aca cgc gct ctg ctc	2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
665 670 675 680	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
685 690 695	
aag agt gcc acc ggt ctc agt aat att ttc tgg gac aag aaa gac gcc	2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
700 705 710	
ggg cag tat atg cga tgc aaa aca ggt atg cag tgg att tgc cat gcc	2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
715 720 725	

atg tca aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc	2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
730 735 740	
gct gaa att gag cag tgg gca tca ggc tgt aca gta cga tag gcc tgg	2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
745 750 755 760	
ggc gcc gtg ttc cga agc aaa aac gtg gtg gtt tgg tta ccg aca acc	2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr	
765 770 775	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
780 785 790	
gca ttg gcc gaa aat cct atc ctg gcc tac tat agc aag ata gtc ttc	2496
Ala Leu Ala Glu Asn Ser Ile Ser Gly Tyr Tyr Ser Lys Ile Val Phe	
795 800 805	
gta tgg gac aag ccg tgg tgg ccc gaa caa gcc ttc tgg gcc gtc ctc	2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
810 815 820	
caa tgg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atr gac	2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
825 830 835 840	
gtc gat cga caa tgg tcc att aac tgt ttc atg gtc gga gac ccg gga	2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
845 850 855	
ccg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
860 865 870	
gac caa ctc ccg gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
875 880 885	
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa	2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
890 895 900	
gga gct ccg agc gcc gtc tat gcc ctg aac gat ctc atc aca ctg ggt	2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
905 910 915 920	
tgg gcc ctc aya aoc ccg ttc aag agt gtt cat ttc gtt gga aoc gag	2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
925 930 935	
aoc tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt	2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
940 945 950	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	2976

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 955 960 965

00100 27  
 00110 991  
 00110 PRT  
 00110 Unknown

00110  
 00110 signal:BEST1 mature:spacer:K:trAPAO (Exophiala spinifera)

00110  
 00110 misc\_feature  
 00110 (1546)..(1534)  
 00110 spacer sequence

00110  
 00110 misc\_feature  
 00110 (1535)..(2973)  
 00110 K:trAPAO

00110  
 00110 misc\_feature  
 00110 (1535)..(1537)  
 00110 Extra lysine

00110 27

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 -20 -15 -10

Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
 -5 -1 1 5

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
 10 15 20

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro  
 25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
 45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
 60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
 75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
 90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
 105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
 125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
 140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
 155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
 170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
 185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
 205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
 220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
 235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
 250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
 265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
 285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly  
 300 305 310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala

315

320

325

Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
 330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
 345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
 365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly  
 380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
 395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
 410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
 425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
 445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
 460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
 475 480 485

Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 490 495 500

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 505 510 515 520

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 525 530 535

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 540 545 550



Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 555 560 565

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 570 575 580

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 585 590 595 600

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 605 610 615

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 620 625 630

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 650 655 660

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
 665 670 675 680

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
 685 690 695

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
 700 705 710

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
 715 720 725

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
 730 735 740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
 745 750 755 760

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
 765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
730 735 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
810 815 820

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
845 850 855

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
860 865 870

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
875 880 885

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
890 895 900

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
905 910 915 920

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
940 945 950

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
955 960 965

0110 28  
0111 3618  
0112 DNA  
0113 Unknown

0220  
0223 gst:espl:sp:K:trAPAO (Exophiala spinifera)

atg	tcc	cct	ata	ctt	ggg	tat	tgg	aaa	att	aag	ggc	ctt	gtg	caa	45
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	
				-215					-220					-215	
ccc	act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	gaa	aaa	tat	gaa	gag	90
Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	
				-210					-205					-200	
cat	ttg	tat	gag	ccc	gat	gaa	ggg	gat	aaa	tgg	cga	aac	aaa	aag	135
His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	
				-195					-190					-185	
ttt	gaa	tgg	ggg	ttg	gag	ttt	ccc	aat	ctt	ccc	tat	tat	att	gat	180
Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	
				-180					-175					-170	
ggt	gat	gtt	aaa	tta	aca	cag	tct	atg	ggc	atc	ata	cgt	tat	ata	225
Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	
				-165					-160					-155	
gat	gac	aag	cac	aac	atg	ttg	ggg	ggg	tgt	cca	aaa	gag	cgt	gca	270

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala	
-150	-145 -140
gag att tca atg ctt gaa gga ggg gtt tgg gat att aga tac ggt	315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly	
-135	-130 -125
gtt tgg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt	360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val	
-120	-115 -110
gat ttt ctt agc aag cta cct gaa atg cgg aaa atg ttc gaa gat cgt	405
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg	
-105	-100 -95
tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac	450
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp	
-90	-85 -80
ttc atg ttg cat gac gat ctt gat gtt gtt tta tac atg gac cca atg	500
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	
-75	-70 -65
tgc cgg gat ggg ttc cca aaa tta gtt cgt ttt aaa aaa cgt att gaa	550
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu	
-60	-55 -50
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca	600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala	
-45	-40 -35 -30
tgg cct ttg bag ggc tgg caa gcc aag ttt ggt ggt ggc gac cat cct	645
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro	
-25	-20 -15
cca aaa tgg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act	690
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr	
-10	-5 -1 1
gtc aag att gat gct ggg atg gtg gtc gcc aag act act act gtc ccc	740
Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro	
5	10 15
ggc acc act ggc acc gtc agc gag ttc ttc ggc gtt cct ttt gcc gcc	790
Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala	
20	25 30 35
tct ccg aca cga ttt ggc cct cct act cgt ccc gtg cct tgg tca acc	840
Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr	
40	45 50
cct ttg caa gcc act gca tat ggt cca gca tgc cct caa caa ttc aat	888
Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn	
55	60 65
tac ccc gaa gaa ctc cgt gag att acg atg gcc tgg ttc aat aca ccg	936
Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro	

70	75	80	
ccc ccg tca gct ggt gaa agt gag gac tgc ctg aac ctc aac atc tac Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr 35 90 95			984
gtc cca gga act gag aac aba aac aaa gcc gtc atg gtt tgg ata tac Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr 100 105 110 115			1032
ggt gga ggg ctg aaa tat ggt tgg aat tca ttc cac att tac gac ggg Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly 120 125 130			1060
gct agt ttc gca gcc aat gag gat gtc atc gcc gtg acc atc aac tac Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr 135 140 145			1128
aga acg aac att ctg ggg ttc cct ggt gcc cct cag att cca ata aca Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr 150 155 160			1176
cag cga aat ctg ggg ttc ata gac caa agg ttt gct ttg gat tgg gta Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val 165 170 175			1224
cag cgg aac atc gca gcc ttt ggc ggt gat cct cga aag gtc aca ata Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile 180 185 190 195			1272
ttt ggg cag agt ccg ggg ggc aga agt gtc gac gtc ctc ttg acg tct Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser 200 205 210			1320
atg cca cac aac cca ccc ttc cga gca gca atc atg gag tcc ggt gtg Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Gln Ser Gly Val 215 220 225			1368
gct aac tac aac ttc ccc aag gga gat ttg tcc gaa cct tgg aac acc Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr 230 235 240			1416
act gtt caa gct ctc aac tgt acc acc agt atc gac atc ttg agt tgt Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys 245 250 255			1464
atg aga aga gtc gat ctc gcc act ctg atg aac acg atc gag caa ctc Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Gln Gln Leu 260 265 270 275			1512
gga ctt ggg ttt gag tac aag ttg gac aac gta acg gct gtg tac cgt Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg 280 285 290			1560
tct gaa acg gct cgc aag act ggt gac att gct cgt gta cct gtt ctc Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu 295 300 305			1608

gtc ggg acg gtg ggc aac gac gga ctt ctc ttt gtc ctc ggg gag aat Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn 310 311 320	1656
gac acc caa gca tat ctc gag gac gca atc ccg aat cag ccc gag ctt Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu 325 330 335	1704
tac cag act ctc ctt gga gca tat ccc att gga tcc cca ggg atc gga Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly 340 345 355	1752
tgg cct caa gat cag att gcc gcc att gag acg gag gta aga ttc cag Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln 360 365 370	1800
tct cct tot gcc atc gtg gct cag gac tcc cgg aat cgg ggt atc cct Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro 375 380 385	1848
tct tgg cgg tac tac tac aat gcc acg ttt gag aat ctc gag ctt ttc Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe 390 395 400	1896
cct ggg tcc gaa gtg tac cac agc tot gaa gtc ggg atc gtg ttt gcc Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly 405 410 415	1944
acg tat cct gtc gca agt gcc acc gcc ttg gag gcc cag acg agc aaa Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys 420 425 430 435	1992
tac atg cag ggt gcc tgg gcc gcc ttt gcc aaa aac ccc atg aat ggg Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly 440 445 450	2040
cct ggg tgg aaa caa gtg ccg aat gtc gcc gcc ctt gcc tca cca gcc Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly 455 460 465	2088
aaa gcc atc cag gtt gac gtc tot cca gcc aca ata gac caa cga tgt Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys 470 475 480	2136
gcc ttg tac acg cgt tat tat act gag ttg ggc aca atc gcc ccg agg Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg 485 490 495	2184
aca ttt ggc gga gcc agc gcc gga gcc agc gcc gga gcc agc aaa gac Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp 500 505 510 515	2232
aac gtt gcc gac gtg gta gtg gtg gcc gct gcc ttg agc ggt ttg gag Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu 520 525 530	2280

acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag	2323
Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu	
535 540 545	
ggg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt acc	2372
Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro	
550 555 560	
ggc agg acg act atc aac gac ctc ggc gat gcg cgg atc aat gac agc	2424
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser	
565 570 575	
aac caa aga gaa gta tcc aga ttg ttt gaa aga ttc cat ttg gag ggc	2472
Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly	
580 585 590 595	
gag ctc cag agg acg act gga aat tcc atc cat caa gca caa gac ggt	2520
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly	
600 605 610	
aca acc act aga gct cct tat ggt gac tcc ttg ctg agc gag gag gtt	2568
Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val	
615 620 625	
gca agt gca ctt ggc gaa ctc ctc ccc gta tgg cct cag ctg atc gaa	2616
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu	
630 635 640	
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc	2664
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu	
645 650 655	
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct	2712
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro	
660 665 670 675	
gct gtt ctc gcc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg	2760
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val	
680 685 690	
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt	2808
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser	
695 700 705	
gcc acc ggt ctc agt aat att ttc tog gac aag aaa gac gcc ggg cag	2856
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln	
710 715 720	
tat atg cga tgc aaa aca ggt atg cag tog att tgc cat gcc atg tca	2904
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser	
725 730 735	
aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc gct gaa	2952
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
740 745 750 755	
att gag cag tog gca tcc gcc tgt aca gta cga tog gcc tog gcc gcc	3000

Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala		
				760					765					770			
gtg	ttc	cga	agg	aaa	aag	gtg	gig	gtt	tgg	tta	ccg	aca	acc	ttg	tat	3048	
Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr		
			775					780					785				
ccc	acc	ttg	aca	ttt	tca	cca	cat	att	ccc	gcc	gag	aag	caa	gca	ttg	3096	
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu		
		790					795				800						
ggg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agg	aag	ata	gtc	ttc	gta	tgg	3144	
Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp		
	805					810					815						
gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tgg	ggc	gtc	ctc	caa	tgg	3192	
Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser		
	820				825				830					835			
agc	tct	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agg	atc	gac	gtc	gat	3240	
Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp		
			840						845					850			
cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	egg	aag	3288	
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys		
			855					860					865				
tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	3336	
Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln		
		870					875					880					
ctc	cgc	gca	gcc	tac	gag	aac	goc	ggg	goc	caa	gtc	cca	gag	ccg	goc	3384	
Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala		
	885					890					895						
aac	gtg	ctc	gaa	atc	gag	tgg	tgg	aag	cag	cag	tat	ttc	caa	gga	gct	3432	
Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala		
	900				905						910				915		
ccg	agg	goc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tgg	ggg	3480	
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala		
				920					925					930			
ctc	aga	aag	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	3528	
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser		
			935					940					945				
tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	goc	ata	cga	tgg	ggt	caa	cga	3576	
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg		
		950						955					960				
ggt	gct	gca	gaa	gtt	gtg	gct	agg	ctg	gtg	cca	gca	gca	tag			3618	
Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala					
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<210> 29



0211> 1205  
 0212> PRT  
 0213> Unknown

0220>  
 0225> gus:espi:sp:K:trAPAO (Exophiala spinifera)

0229>  
 0231> misc\_feature  
 0232> (1)..(627)  
 0233> gus + polylinker

0236>  
 0238> misc\_feature  
 0239> (191)..(2226)  
 0239> spacer sequence

0239>  
 0241> misc\_feature  
 0242> (2227)..(3615)  
 0243> K:trAPAO

0250>  
 0251> misc\_feature  
 0252> (2227)..(2229)  
 0253> extra lysine

0400> 29

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln
				-225				-220						-215

Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu
			-210					-205						-200

His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys
			-195					-190						-185

Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp
			-180					-175						-170

Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile
			-165					-160						-155

Ala	Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala
			-150					-145						-140

Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly
			-135					-130						-125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
 -120 -115 -110  
 Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg  
 -105 -100 -95  
 Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp  
 -90 -85 -80  
 Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met  
 -75 -70 -65  
 Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu  
 -60 -55 -50  
 Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala  
 -45 -40 -35 -30  
 Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro  
 -25 -20 -15  
 Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr  
 -10 -5 -1 1  
 Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro  
 5 10 15  
 Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala  
 20 25 30 35  
 Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr  
 40 45 50  
 Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn  
 55 60 65  
 Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro  
 70 75 80  
 Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr  
 85 90 95  
 Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr

100

105

110

115

Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly  
 120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr  
 135 140 145

Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr  
 150 155 160

Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val  
 165 170 175

Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile  
 180 185 190 195

Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser  
 200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val  
 215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr  
 230 235 240

Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys  
 245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu  
 260 265 270 275

Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg  
 280 285 290

Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu  
 295 300 305

Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn  
 310 315 320

Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu  
 325 330 335

Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly  
 340 345 350 355

Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln  
 360 365 370

Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro  
 375 380 385

Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe  
 390 395 400

Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly  
 405 410 415

Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys  
 420 425 430 435

Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly  
 440 445 450

Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly  
 455 460 465

Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys  
 470 475 480

Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg  
 485 490 495

Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp  
 500 505 510 515

Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu  
 520 525 530

Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu  
 535 540 545

Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro  
 550 555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser  
565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly  
580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly  
600 605 610

Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val  
615 620 625

Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu  
630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu  
645 650 655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro  
660 665 670 675

Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val  
680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser  
695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln  
710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser  
725 730 735

Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu  
740 745 750 755

Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala  
760 765 770

Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr  
775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu  
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp  
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser  
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp  
840 845 850

Asp Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys  
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln  
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala  
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala  
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala  
920 925 930

Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser  
935 940 945

Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
950 955 960

Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
965 970 975

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<211> 3591  
<212> DNA  
<213> Unknown

<220>  
<223> Orf of BEST1:K:trAPAO fusion pGEX-4T-1 (Exophiala spinifera)  
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0221> misc\_feature  
 0222> (1)..(637)  
 0223> gst + polylinker

0224>  
 0225> mat\_peptide  
 0226> (638)..(2163)  
 0227> BBST1 mature

0228>  
 0229> misc\_feature  
 0230> (2164)..(2199)  
 0231> spacer sequence

0232>  
 0233> misc\_feature  
 0234> (2200)..(3333)  
 0235> KtrAPAO

0236>  
 0237> CDS  
 0238> (1)..(3583)  
 0239>

0240>  
 0241> misc\_feature  
 0242> (2400)..(2432)  
 0243> extra lysine

0400> 30  
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa 45  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln  
 -225 -220 -215  
  
 ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag 90  
 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
 -210 -205 -200  
  
 cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag 135  
 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
 -195 -190 -185  
  
 ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat 180  
 Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
 -180 -175 -170  
  
 ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata 225  
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
 -165 -160 -155  
  
 ggt gac aag cac aac atg ttg ggt ggt tct cca aaa gag cgt gca 270  
 Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala

	-150	-145	-140	
gag att tca atg ctt gaa gga ggg gtt ttg gat att aga tac ggt				315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly				
	-135	-130	-115	
gtt tgg aga att gga tat agt aaa gac ttt gaa act ctc aaa gtt				360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val				
	-120	-115	-110	
gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt				405
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg				
	-105	-100	-95	
cta tgt cat aaa acc tat tta aat gct gat cat gta acc cat cct gac				450
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp				
	-90	-85	-80	
ctc atg ttg tat gag gct ctt gat gtt gtt tta tac atg gac cca atg				504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met				
	-75	-70	-65	
tgc ctg gat ggg ttc cca aaa tta gtt tct ttt aaa aaa cgt att aaa				558
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu				
	-60	-55	-50	
gct atc cca cca att gat aag tac ttg aaa tcc agc aag tat ata gga				600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala				
	-45	-40	-35	
ttg cct ttg cag ggc tgg cca gcc aag ttt ggt ggt ggc gac cat cct				648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro				
	-25	-20	-15	
cca aaa tgg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt				696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe				
	-10	-5	-1 1	
ccg gtc cgc agc aac gat ctg ggc cag gtt cag gga ctg gcc ggg gac				744
Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp				
	5	10	15	
gtg atg agc ttt cgc gga ata ccc tat gca ggc ccg ccg gtg ggc ggg				792
Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly				
	20	25	30	
ctg cgt tgg aag ccg ccc caa cac gcc cgg ccc tgg gcc gcc gtt cgc				840
Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg				
	40	45	50	
ccc gcc acc caa ttt ggc tcc gac tgc ttc ggc ggc gcc tat ctt cgc				888
Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg				
	55	60	65	
aaa ggc agc ctc gcc ccc ggc gtg agc gag gac tgt ctt tac ctc aac				936
Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn				
	70	75	80	



gta tgg ggg cgg tca ggc ggt aaa ccc ggc cag tac ccc gtc atg gtc	384
Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val	
85 90 95	
tgg gtc tac ggc ggc ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac	1032
Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr	
100 105 110 115	
tac gac ggc gag ggg ctt ggg cga cag ggc gtc gtc gtc gtc acg ttt	1080
Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe	
120 125 130	
aac tat cgg acg aac atc ctg ggc ttt ttc gcc cat cct ggt ctc tog	1128
Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser	
135 140 145	
cgc gag agc ccc acc gga act tog ggc aac tac ggc cta ctc gac att	1176
Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile	
150 155 160	
ctc gcc gct ctt cgg tgg gtc cag agc aac gcc cgc gcc ttc gga ggc	1224
Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly	
165 170 175	
gac ccc ggc cga gtc acg gtc ttt ggt gaa tog gcc gga ggc agc gcc	1272
Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala	
180 185 190 195	
atc gga ctt ctg ctc aac tog cgg ctg agc aag ggt ctc ttc cgt ggc	1320
Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly	
200 205 210	
gct atc ctc gaa agt cca ggg ctg acg cga cgg ctc gcc acg ctc gcc	1368
Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala	
215 220 225	
gac agc gcc gcc tog ggc gag cgc ctc gac gcc gat ctt tog cga ctg	1416
Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu	
230 235 240	
cgc tog acc gac cca gcc aac ctg atg ggc cgc gcc gac gcc gcc cgc	1464
Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg	
245 250 255	
cgg gca tog cgg gac ctg cgc agc cgg cgt cgg acc gga cgg atc gtc	1512
Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val	
260 265 270 275	
gat ggc cat gtc ctg cgg cag acc gac agc gcc gcc atc gcc gcc ggc	1560
Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly	
280 285 290	
cag ctg gcc cgg gtt cgg gtc ctg atc gga acc aat gcc gac gaa ggc	1608
Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly	
295 300 305	

egg gcc ttc ctc ggg ggc ggg cgg atg gag acg cca ggg gac tac caa Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln 310 315 320	1656
gcc tat ctg gag ggc gag ttc ggc gac caa gcc gcc gcc gtg ggc ggc Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Val Ala Ala 325 330 335	1704
tgc tat ccc ctc gac ggc ggg gcc acg ccc aag gaa atg gtc ggc ggc Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg 340 345 350 355	1752
atc ttc ggc gac aat cag ttc aat cgg ggg gtc tgg gcc ttc tgg gaa Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu 360 365 370	1800
ggg ctt ggc ggc gag ggc ggc ccc gtc tgg ctt tat cag ttc aac ggt Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly 375 380 385	1848
aat acc gag ggt gga aga ggc cgg gct acc ctc gga gcc gaa att ccc Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro 390 395 400	1896
tac gtt ttc ggg gtc ttc aag ctc gac gag ttc ggt ctg ttc gat tgg Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp 405 410 415	1944
cgg ccc gag ggg ccc aag ccc gcc gac cgt ggc ctg gcc caa ctg atg Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met 420 425 430 435	1992
tcg tcc gcc tgg gtc cgg ttc gcc aag aat gtc gac ccc gcc ggg gac Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp 440 445 450	2040
gcc ctt acc tgg cct gcc tat tct aag ggc aag tgg acc atg aca ttc Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe 455 460 465	2088
ggt ccc gag ggc cgc ggc ggc gtc gtc tgg ccc gga cct tcc atc ccc Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro 470 475 480	2136
cct tgc ggc gat ggc gcc aag ggc ggc ggc gga ggc agc ggc gga ggc Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly 485 490 495	2184
agc ggc gga ggc agc aaa gac aac gtt ggc gac gtc gta gtc gtc ggc Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly 500 505 510 515	2232
gct gcc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 520 525 530	2280
ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta ggg gga aag act	2328

Leu Ser Cys	Leu Val	Leu Glu	Ala Met	Asp Arg	Val Gly	Gly Lys	Thr	
535			340			545		
ctg agc gta	caa tog	ggg ccc	ggc agg	agg act	atc aac	gac ctc	ggc	2376
Leu Ser Val	Gln Ser	Gly Pro	Gly Arg	Thr Thr	Ile Asn	Asp Leu	Gly	
550			555			560		
gct ggg tgg	atc aat	gac agc	aac caa	agc gaa	gta tcc	aga ttc	ttt	2424
Ala Ala Trp	Ile Asn	Asp Ser	Asn Gln	Ser Glu	Val Ser	Arg Leu	Phe	
565			570			575		
gaa aya ttt	cat ttg	gag ggc	gag ctc	cag agg	acg act	gga aat	tca	2472
Glu Arg Pro	His Leu	Gln Gly	Glu Leu	Gln Arg	Thr Thr	Gly Asn	Ser	
580		585		590		595		
atc cat caa	gaa caa	gac ggt	aca acc	act aca	gct cct	tat gct	gac	2520
Ile His Gln	Ala Gln	Asp Gly	Thr Thr	Thr Thr	Ala Pro	Tyr Gly	Asp	
	600		605			610		
tcc ttg ctg	agc gag	gag gtt	gaa agt	gaa ctt	ggg gaa	ctc ctc	ccc	2568
Ser Leu Leu	Ser Glu	Gln Val	Ala Ser	Ala Leu	Ala Glu	Leu Leu	Pro	
	615		620			625		
gta tgg tct	cag ctg	atc gaa	gag cat	agc ctt	caa cac	ctc aag	ggg	2616
Val Trp Ser	Gln Leu	Ile Glu	Glu His	Ser Leu	Gln Asp	Leu Lys	Ala	
	630		635			640		
agc cat cag	ggg aag	ggg ctc	gac agt	gtg agc	ttc ggg	cac tac	tgt	2664
Ser Pro Gln	Ala Lys	Arg Leu	Asp Ser	Val Ser	Phe Ala	His Tyr	Cys	
	645		650		655			
gag aag gaa	cta aac	ttg cct	gct gtt	ctc ggc	gta gca	aac cag	atc	2712
Glu Lys Glu	Leu Asn	Leu Pro	Ala Val	Leu Gly	Val Ala	Asn Gln	Ile	
660		665		670		675		
aca cgg gct	ctg ctc	ggt gtg	gaa gcc	cac gag	atc agc	atg ctt	ttt	2760
Thr Arg Ala	Leu Leu	Gly Val	Gln Ala	His Glu	Ile Ser	Met Leu	Phe	
	680		685			690		
ctc acc gac	tac atc	aag agt	gcc acc	ggt ctc	agt aat	att ttc	tog	2808
Leu Thr Asp	Tyr Ile	Lys Ser	Ala Thr	Gly Leu	Ser Asn	Ile Phe	Ser	
	695		700			705		
gac aag aaa	gac ggc	ggg cag	tat atg	cga tgc	aaa aca	ggt atg	cag	2856
Asp Lys Lys	Asp Gly	Gly Gln	Tyr Met	Arg Cys	Lys Thr	Gly Met	Gln	
	710		715			720		
tgg att tgc	cat gcc	atg tca	aag gaa	ctt gtt	cca gcc	tca gtg	cac	2904
Ser Ile Cys	His Ala	Met Ser	Lys Glu	Leu Val	Pro Gly	Ser Val	His	
	725		730		735			
ctc aac acc	ccc gtc	gct gaa	att gag	cag tog	gca tcc	ggc tgt	aca	2952
Leu Asn Thr	Pro Val	Ala Glu	Ile Glu	Gln Ser	Ala Ser	Gly Cys	Thr	
740		745		750		755		
gta cga tog	gcc tog	ggc gcc	gtg ttc	cga agc	aaa aag	gtg gtg	gtt	3000
Val Arg Ser	Ala Ser	Gly Ala	Val Phe	Arg Ser	Lys Lys	Val Val	Val	

760										765					770					
tgg	tta	cgg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	3043				
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu					
775					780					785										
ccc	gac	gag	aag	caa	gca	ttg	gag	gaa	aat	tct	atc	ctg	ggc	tac	tat	3096				
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr					
790					795					800										
agg	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	ggc	gaa	caa	ggc	3144				
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly					
805					810					815										
ttc	tgg	ggc	gtc	ctc	caa	tgg	agg	tgt	gac	ccc	atc	tca	ttt	ggc	aga	3192				
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg					
820					825					830					835					
cat	acc	agg	atc	gac	gtc	gat	agg	caa	tgg	tcc	att	acc	tgt	ttc	atg	3240				
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met					
840					845					850										
gtc	gga	gac	ccg	gga	agg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	agg	3288				
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg					
855					860					865										
caa	aag	tct	gtc	tgg	gac	caa	ctc	agg	gca	ggc	tac	gag	aac	ggc	ggc	3336				
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly					
870					875					880										
ggc	caa	gtc	cca	gag	ccg	ggc	aac	gtg	ctc	gaa	atc	gag	tgg	tgg	aag	3384				
Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys					
885					890					895										
cag	cag	tat	ttc	caa	gga	gct	ccg	agg	ggc	gtc	tat	ggg	ctg	aac	gat	3432				
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp					
900					905					910					915					
ctc	atc	aca	ctg	ggg	tgg	ggg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	3480				
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His					
920					925					930										
ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	3528				
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly					
935					940					945										
ggc	ata	aga	tgg	ggg	caa	aga	ggg	gct	gca	gaa	gtt	gtg	gct	agg	ctg	3576				
Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu					
950					955					960										
gtg	cca	gca	gca	tag												3591				
Val	Pro	Ala	Ala																	
965																				

0210> 31  
0211> 1196

4213: PRT  
 4214: Unknown

4200:  
 4201: Ord of BEST1:K:trAPAO fusion pGEX-4T-1 (Exophiala spinifera)

4100:  
 4110: misc\_feature  
 4111: (1)..(637)  
 4100: gst + polylinker

4100:  
 4110: misc\_feature  
 4111: (2164)..(2199)  
 4100: spacer sequence

4100:  
 4110: misc\_feature  
 4111: (2200)..(3538)  
 4100: K:trAPAO

4100:  
 4110: misc\_feature  
 4111: (2000)..(2200)  
 4100: extra lysine

4400: 31

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln  
 -225 -220 -215

Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
 -210 -205 -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
 -195 -190 -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
 -180 -175 -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
 -165 -160 -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
 -150 -145 -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
 -135 -130 -125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val

-120

-115

-110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg  
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp  
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met  
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu  
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala  
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro  
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe  
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp  
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly  
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg  
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg  
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn  
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val  
85 90 95

Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr  
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe  
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser  
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile  
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly  
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala  
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly  
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala  
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu  
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg  
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val  
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly  
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly  
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln  
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala  
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg  
 340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu  
 360 365 370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly  
 375 380 385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro  
 390 395 400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp  
 405 410 415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met  
 420 425 430 435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp  
 440 445 450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe  
 455 460 465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro  
 470 475 480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly  
 485 490 495

Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
 500 505 510 515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
 520 525 530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
 535 540 545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
 550 555 560



Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
 565 570 575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
 580 585 590 595

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp  
 600 605 610

Ser Leu Leu Ser Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
 615 620 625

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
 630 635 640

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
 645 650 655

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
 660 665 670 675

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
 680 685 690

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
 695 700 705

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
 710 715 720

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
 725 730 735

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
 740 745 750 755

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
 760 765 770

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
 775 780 785

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr

790

795

800

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
 805 810 815

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
 820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
 840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
 855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
 870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
 885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
 900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
 920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
 950 955 960

Val Pro Ala Ala  
 965

\*010\* 38  
 \*011\* 1803  
 \*012\* DNA  
 \*013\* Unknown

\*020\*  
 \*023\* Glyc(-) mutation in glycosylation sites (Exophiala spinifera)

\*020\*  
 \*021\* CDS

(1222) (1) (1803)

(1223)

(1400) 32

atg	gca	ctt	gca	ccg	agc	tac	atc	aat	ccc	cca	aac	gtc	gca	tcg	cca	18
Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro	
1				5				10						15		

gca	ggg	tat	tct	cac	gtc	ggc	gta	ggc	cca	gac	gga	ggg	agg	tat	gtg	36
Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val	
			20					25						30		

aca	ata	gct	gga	cag	att	gga	caa	gac	gct	tgg	ggc	gtg	aca	gac	cct	144
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro	
		35					40							45		

acc	tac	gag	aaa	cag	gtt	gac	caa	gca	ttc	gac	aac	ctg	cga	gct	tgc	192
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	
	50					55					60					

ctt	gct	gca	gtt	gga	gac	act	tca	aac	gac	gtc	acc	aag	ctc	aat	tac	240
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr	
65						70					75				80	

tac	atc	gtc	gac	tac	gac	ccg	agc	aaa	ctc	acc	gca	att	gga	gac	ggg	288
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	
			85						90						95	

ctg	aag	gct	acc	ttt	gac	ctt	gac	agg	ctc	cct	cct	tgc	acg	ctg	gtg	336
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	
		100						105						110		

cca	gtg	tgg	gac	ttg	tct	tca	cct	gaa	tac	ctc	ttt	cag	gtt	gat	gac	384
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	
		115					120						125			

acg	gag	ctg	gtg	ccg	gga	cac	acg	acc	cca	gac	aac	gtt	gag	gac	gtg	432
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	
		130				135						140				

gta	gtg	gtg	ggc	gct	ggc	tgg	agc	ggc	ttg	gag	acg	gca	cgc	aaa	gtc	480
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	
145					150					155					160	

cag	gac	gac	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gag	atg	gat	cgt	gta	528
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	
			165						170					175		

ggg	gga	aag	act	ctg	agc	gta	caa	tgg	ggt	ccc	ggc	agg	acg	act	atc	576
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	
		180						185					190			

aac	gac	ctc	ggc	gct	ggc	tgg	atc	aat	gat	agc	aac	cag	gac	gaa	gta	624
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ala	Glu	Val	
		195				200							205			

tcg	aga	ttg	ttt	gaa	aga	ttt	cac	ttg	gag	ggc	gag	ctc	cag	agg	acg	672
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	
210						215					220					
act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	720
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	
225					230				235						240	
act	tat	ggt	gac	tcc	ttg	ctg	agg	gag	gag	gtt	gca	agt	gca	ctt	gag	768
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Gln	Glu	Val	Ala	Ser	Ala	Leu	Ala	
				245					250					255		
gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gac	gag	cat	agg	ctt	caa	-16
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	
			260					265					270			
gac	ctc	aag	gag	agg	cat	cag	ggg	aag	ggg	ctc	gac	agt	gtg	agg	ttc	864
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	
		275					280					285				
ggg	caa	tac	tgt	gag	aag	gaa	cta	aac	ttg	cat	gct	gtt	ctc	ggc	gta	912
Ala	His	Tyr	Cys	Gln	Lys	Gln	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	
	290				295						300					
gca	aac	cag	atc	aca	ggc	ggt	ctg	ctc	ggt	gtg	gaa	goc	caa	gag	atc	960
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	
305					310				315						320	
agg	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	goc	acc	ggt	ctc	agt	1008
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	
				325					330					335		
aat	att	ttc	tgg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	1056
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	
			340					345					350			
aca	ggt	atg	cag	tgg	att	tgc	cat	goc	atg	tca	aag	gaa	ctt	gtt	cca	1104
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	
			355				360					365				
ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tgg	gca	1152
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	
	370				375					380						
tcc	ggc	tgt	aca	gta	cga	tgg	goc	tgg	ggc	goc	gtg	ttc	cga	agg	aaa	1200
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	
385					390				395						400	
aag	gtg	gtg	gtt	tgg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	1248
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	
				405					410					415		
tca	cca	cat	ctt	ccc	goc	gag	aag	caa	gca	ttg	ggg	gaa	aat	tct	atc	1296
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	
			420				425						430			
ctg	ggc	tac	tat	agg	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	1344
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	

435

440

445

cgc gaa caa gcc ttc tgc gcc gtc ctc caa tgc agc tgt gac gcc atc 1392  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att 1440  
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc 1488  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Glu Gln Ser  
 485 490 495

cag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac 1536  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510

cag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525

cag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540

cgg ctg aac gat ctc atc aca ctg ggt tgc gcc ctc aga acg ccg ttc 1680  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728  
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575

tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt 1776  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590

gtg gct agc ctg gtg cca gca gca tag 1803  
 Val Ala Ser Leu Val Pro Ala Ala  
 595 600

\*210\* 33

\*211\* 600

\*212\* PRT

\*213\* Unknown

\*220\*

\*223\* Glyc(-) APAO; mutation in glycosylation sites (Exophiala spinifera)

\*400\* 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
 1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
 65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
 115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val  
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
 225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala

245

250

255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
 260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
 275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
 325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
 370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
 420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
 435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<210> 34  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 37-mer oligonucleotide (Exophiala spinifera)

<400> 34  
 ggggaattca tggcacttgc accgagctac atcaatc

37

<210> 35  
 <211> 1929  
 <212> DNA  
 <213> Exophiala spinifera

<220>  
 <221> Intron  
 <222> (739)..(811)  
 <223>

<220>



<221> Intron  
 <222> (1134)..(1186)  
 <223>

<400> 35  
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 caaatcgggc taggcccata cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120  
 gagggttttg ggttgacaga cccagcctac gagaaacagg ttgcacaagc attcgccaat 180  
 ctggagagctt gcttgctgc agttggagcc tcttcacacg acgtcaccaa gctcaattac 240  
 taatcgctcg actaaccccc gagcaaacctc ccgcgaattg gagatgggct gaagtctacc 300  
 tctgcctctg acaggctccc tcttgcacg ctggtgcacg taacggcctt ggcttcacct 360  
 gaataacctc ttgaggttga tgcaacggcg ctggtgcacg gacactcgac ccagacaaac 420  
 gttgcgggacg ttgtagtgtt gggcgctggc ttgagcggtt tggagacggc acccaaaagtc 480  
 caggcgcgcg gtctgtctcg cctcgctctt gaggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtac aatcggttcc cggcaggacg actatcaacg acctcggcgc tgggtggatc 600  
 aatgacagca accaaaagca agtatccaga ttgtttgaaa gatttcattt ggaggggcag 660  
 ctccagagga cgaacggaaa tccaatccat caagcacacg accgtacaaac cactacagct 720  
 ccttatggtg actcccgggt aagcacaaac ccactttgtg atgagacctc tgtcgagtgt 780  
 agaatacagt cactgaactc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840  
 ggaactcttc cccgtatggt ctcaagctgat cgaagagtat agccttgaag accccaaggc 900  
 gagecctcag gcgaaagcggc tcgacagtgt gaccttcgag cactactgtg agaaggacct 960  
 aaaacttgcct gctgttctca ggttgacaaa ccagatccac cgcgctctgc tgggtgtgga 1020  
 agcccacgag atcagcatgc tttttctcac cgaactacac aagagtgcac ccggtctcag 1080  
 taatattgtc tcggacaaag aagaacggcg gcagtatatg cgatgcaaaa caggtgcgtg 1140  
 cgggtctctc tcaggtaggg gaactgttct ttagtggtca tccagggtat gcagtgcatt 1200  
 tgccatgcca tgcacaaagg aattgttcca ggtcagtg cactcaaac acccgctcgt 1260  
 ggaattgagc agtcggcgct cggctgtata gtaacgatcg cctcgggcgc cgtgttccga 1320  
 agcaaaaagg ttgtgggttc gttaccgaca acattgtatc ccacctgac attttacca 1380  
 cctcttcccg ccgagaagca agcattggcg gaaaaatcta cctcggcta ctatagcaag 1440  
 atagtcttcg tatgggacaa cccgtggtgg ccgcaacaag gcttctcggg cgtcctccaa 1500  
 tcgagctgtg acccatctc atttgcacg gataccagca tcgaagtga tcggcaatgg 1560

tccattacct gtttcattggt cggagaccgg ggaagggaagt ggtcccaaca gtccaagcag 1620  
 gtaacacaaa agtctgtctg ggaccaactc cggcagacct acgagaaagg cggggcccaa 1630  
 gtccagagac cggccaacgt gctgaaatc gagggttoga agcagcagta tttccaagga 1740  
 gctccgagcg ccgtctatgg gctgaacgat ctcacacac tgggttcggc gctcagaacg 1800  
 ccgtcaagt ggttcattt cgttggaacg gagacgtctt tagtttggaa agggatatg 1850  
 gaaggggcca taagatcggg tcaacgaggt gctgcagaag ttgtggetag cctggtgcca 1920  
 gtagatag 1929

0210 36  
 0211 600  
 0212 PBT  
 0213 Exophilia spinifera

0400 36

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
 1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val  
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro  
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr  
 65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
 115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
 225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
 260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
 275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
 325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala

(110) 37  
 (111) 1929  
 (112) DNA  
 (113) *Exophiala spinifera*

(110)  
 (111) Intron  
 (112) (789)..(811)  
 (113)

(110)  
 (111) Intron  
 (112) (1134)..(1136)  
 (113)

(110) 37  
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 caaatcgggcy taggcccacaa cgaagcgagg talgtgacaa tagctggaca gattggacaa 120  
 gacgctttggc ggttgacaga cccagcctac gagaaacagg ttgcccacagc attcgcacat 180  
 ctgagagctt gctttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240  
 caaatcgtcg actacgcctc gagcaaacctc accgcaattg gagatgggct gaagtctacc 300  
 ttgccccttg acaggctccc tctttgcacg ctggtgcacg taccggcctt ggcttcacct 360  
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 gttgaggacg tggtagtggc gggcgctggc ttgagcggtc tggagacggc acgcaaacgc 480  
 caggccgcgcg gtctgtctct cctcgtctct gaggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtae aatcgggttc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaaagcga agtatccaga ttgtttgaaa gatttcattt ggaggcgag 660  
 ctccagagga cgaacggaaa ttcacacat caagcacaag acggtacaa cactacagct 720  
 ccttatggtg actcccggc aagcacaate ccactctgtg atgagacctc tgtcagtggt 780  
 agaatacagt cactgaactc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840  
 ggaactcttc cccgtatggt ctacgtgat cgaagagtat agccttgaag accccaaggc 900  
 gagcctcag cgaagcggc togacagtgt gagcttcgag cactactgtg agaaggacct 960  
 aaacttgct gctgtctca gctggcaca ccagatcaca cgcgtctgc tgggtgtgga 1020  
 agccacagag atcagcatgc tttttctcac cgactacatc aagagtgcac cgggtctcag 1080  
 taatattgtc tcggacaaga aagacggcg gcagtatatg cgatgcaaaa caggtgcgtg 1140

cgggtgtcttc tcaggttaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt 1200  
 tcccatgcca tgtcaaaagga acttggttca ggtccagtcg acctcaacac ccccgctcgt 1250  
 ggaattgagc agtcggcgctc cggctgtata gtaagatcgg cctcggggcg cgtgttcaga 1300  
 aacaaaaagg tggtagtttc gttacagaca acattgtatc ccaccttgac attttcacca 1350  
 ctctttcccg ccgagaagca agcattggcg gaaaaatcta tctcgggcta ctatagcaag 1400  
 atagtcctcg tatgggacaa cccgtgggtg ccgagaacaag gcttctcggg cgtctctcaa 1450  
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 ccgttcaagt ggttcattt cgttggaacg gagacgtctt tagttcggaa aggggtatcg 1750  
 caaggggcca taagatcggg tcaacgaggt gctgcagaag ttgtggctag cctgggtcca 1800  
 ccagcatag 1829

02100 33  
 02111 600  
 0212 PRT  
 0213 Exophiala spinifera

04000 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

85

90

95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
 325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
 370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
 420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
 435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540



Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<110> 39  
 <111> 1930  
 <112> DNA  
 <113> *Exophiala spinifera*

<220>  
 <221> Intron  
 <222> (739)..(811)  
 <223>

<220>  
 <221> Intron  
 <222> (1134)..(1187)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (649)..(649)  
 <223> n = A,T,C or G

<400> 39  
 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggattttct 60  
 caagtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgcttcgg gcgtgacaga cctgcctac gagaaacagg ttgcccagc attcgccaat 180  
 ctgcgagctt gccttgcctgc agttggagcc acttcaaacy acgtcaccaa gctcaattac 240  
 tacatcgteg actacgcccc gagcaaacct accgcaattg gagatgggct gaaggctacc 300  
 tttgcctttg acaggctccc tctttgcaag ctgggtgcag tgteggcctt gtcttcacct 360  
 gaatacctct ttgaggttga tgccaaggcg ctgggtgcgg gacacacgac ccagacaaac 420  
 gttgaggagc tggtagtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
 caggccggcg gtctgtcctg cctcgcttctt gaggcgatgg atcgtgtagg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag	660
ctccagagga cgaactggaaa ttcaatccat caagcacaag acggtacaa cactacagct	720
ccttatgggtg actccttggg aagcacaatc ccactttgtg atgagacctc tgcagagtgt	780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc	840
ggaaactctc ccggtatggg ctcagctgat cgaagagcat agccttcaag acctcaaggc	900
gagacctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggaaat	960
aaacttgcct gctgttctcg gcttagcaaa ccagatcaca cgcctctctg tcgggtgtga	1020
agcccaagag atcagcatgc tttttctcac cgaactacac aagagtgcac ccggtctcag	1080
caatattttc tcggacaaga aagacggcgg gcagtatatg ccatgcacaa caggtgcgtg	1140
tcggtctctc tcaggtgggg gactcgttcc tcaagtggtc atttcaggta tgcagtcgat	1200
tcgpcatgcc atgtcaaagg aacttgttcc aggcctcagt caccctcaac cccccgtctc	1260
tgaatttgag cagtcggcat ccggctgtac agtacgatcg gcctcggcgc ccgtgttcgc	1320
aagcaaaaag gtgggtgggtt cgttacccac aacctgttat cccacctga cattttcacc	1380
acctctccc gcgcgagaagc aagcattggc ggaaaattct atctgggct actatagcaa	1440
gatagtcttc gtatgggaca agccgtgggt gcgcgaacaa ggcttctcgg gctcctcca	1500
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gtccattacc tgtttcatgg tcggagacc ccggaaggag tggccccaac agtccaagca	1620
ggtaacgaca aagtctgtct gggaccaact ccgcgcagcc tacgagaac ccggggccca	1680
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agctccgagc gccgtctatg ggtgaacga tctcatcaca ctgggttcgg cgtcagaac	1800
gcggttcaag agtggtcatt tcgttggaac ggagacgtct ttagtttgga aagggtatat	1860
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agcagcatag	1980

<210> 40  
 <211> 598  
 <212> PRT  
 <213> *Exophiala spinifera*

<220>  
 <221> MISC\_FEATURE  
 <222> (216)..(216)

(223) Xaa = any amino acid

(400) 40

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
195 200 205

Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr  
 210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro  
 225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
 245 250 255

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
 260 265 270

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
 275 280 285

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn  
 290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
 305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
 325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
 340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
 355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
 370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val  
 385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro  
 405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly  
 420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu

435

440

445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
 450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys  
 465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
 485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn  
 500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
 515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu  
 530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser  
 545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
 565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
 580 585 590

Ser Leu Val Pro Ala Ala  
 595

<210> 41  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocycladiella atrovirens*

<220>  
 <221> Intron  
 <222> (739)..(811)  
 <223>

<220>  
 <221> Intron  
 <222> (1134)..(1185)  
 <223>

<400> 41

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gaagcttcgg	ccgtgacaga	ccctggctac	gagaaacagg	ttgcccagc	attcgccaac	180
ctggagagctt	gtcttgctgc	agtgaggacc	actccaaacg	acattaccaa	gtccaattac	240
tacatcgttcg	actacaaccc	gagcaaaactc	acggcaattg	gagatgggct	gaaggctacc	300
tttgccccttg	acaggctccc	tccttgcaag	ctgggtgcacg	tgccggccct	ggcttcacct	360
gaataccctt	tcgaggctga	tgccaaggcg	ctgggtccag	gacactcaac	cccagacaa	420
gttcgggaag	tggctgtggt	gggagctggc	ctgagcggtt	tggaagcggc	acgcaagtc	480
caggctggcg	ggctgtcttcg	cctcgctctt	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcggttc	cggcaggagc	gcatacaatg	acctcgggcg	tgcgtggatc	600
aatgacagca	acccaaaggc	agtaattcaaa	ttatttgaaa	gattccattt	ggaggggag	660
ctccagagga	cgaacggaaa	ttcaatccat	caagcacaag	acggtaacaac	cactacagct	720
ccttatggcg	attccctggc	aaacacaatt	ccatcttgct	atgagacctc	tgtcgtgtgt	780
agaatacagt	cgtcgaactcc	acatcgtcca	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaaactcctt	cccgcatggt	ctcagctgat	cgaagagcat	agtcttgaa	accccaaggc	900
gagccctcaa	gggaagcgag	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgccct	gctgtctctcg	gctggccaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccaacgag	atcagcatgc	ttttctccac	cgaactacac	aagagtgcac	ccggtctcag	1080
taatatgtgc	toggataaga	aagacggctg	gcagtatatg	cgatgcacaaa	caggtgcgtg	1140
tgggtgtctc	tcagtgggag	actcgtttct	tagtggctac	tcaggtatg	cagtgcctct	1200
gccatgccat	gtcaaaaggaa	cttggtccag	gctcagtgca	cctcaacacc	cccgctcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	taagatcggc	ctcggggcg	gtgttcacgaa	1320
gtaaaaagggt	ggtygtttcg	ttaccgacaa	ccttgctatcc	caaccttgata	ttttcaaccac	1380
ctcttcccg	cgaagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagctcttcgt	atgggacaa	ccgtggctgg	gagaaacagg	cttctcgggc	gtctccaat	1500
cgaagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtogat	cggcaatggt	1560
ccattacctg	tttcatggct	ggagacccgg	gaagggaagt	gtcccaacag	tcacaagcag	1620
tacgacagaa	gtctgtctgg	aaacaaactcc	ggcagagcta	cgaagaacgc	ggggcccaag	1680

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 cgcagagcgt cgtctatggg ctgaactgtc tcaacacact gggcttcggcg ctccagaacgc 1800  
 cgtccaaggg tgttcatttc gttcgaaagg agaagttctt ggtttggaaa gggatatgg 1860  
 aagggggcat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctgggtgcag 1920  
 cagcatag 1928

<210> 42  
 <211> 598  
 <212> PRT  
 <213> *Rhinocycladiella atrovirens*

<400> 42

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro  
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala  
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
 65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala  
 115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr  
225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu  
245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro  
260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His  
275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn  
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380



Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val  
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro  
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly  
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
450 455 460

Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys  
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
485 490 495

Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn  
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu  
530 535 540

Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly  
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
580 585 590

Ser Leu Val Pro Ala Ala  
595

<210> 43  
 <211> 1928  
 <212> DNA  
 <213> Rhinocycladiella atrovirens

<220>  
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 <222> (739)..(811)  
 <223>

<220>  
 <221> Intron  
 <222> (1134)..(1185)  
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<400> 43  
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 gaggtttcgg ccgtgacaga ccttgccatc gagaaacagg ttgcccagc attcggccaa 180  
 ctggcagatt gtattgtctc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
 taacatcgtcg actacaacc gagcaaacctc acgcgaattg gagatggggt gaaggctacc 300  
 tttgcctctg acaggctccc tcttgccaag ctgggtgcacg tgcgggcact ggcttcactt 360  
 gaatacctct ttgaggttga tgcacgggag ctgggttcacg gacactcaac ccagacaaat 420  
 gttgagggaag ttgtcgttgt gggcgctggc ttgagcgggt ttgagacggc acgcaaagtc 480  
 caggctgcag ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaagactt 540  
 ctgacgctac aatcgggttc cggcaggaag actatcaatg acctcgggcg tgcgtggatc 600  
 aatgacagca accaaaagga agtattcaaa ttatttgaaa gatttcattt ggaggggag 660  
 ctccagagga cgaacggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
 ccttatgggtg attcctcgtt aagcacaatt ccctcttggt atgagacctc tctcgtgtgt 780  
 agaatacagt cgtgactcc acatcgtcca gctgagcag gaggttgcaa gtgcactcgc 840  
 ggaactcctt cccgcctggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900  
 gagccctcaa gccaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960  
 aaacttgccg gctgtctctg gctggccaaa ccagatcaca cgcgctctgc tgggtgtgga 1020  
 agcccacag atcagcatgt tttctctcac ggaactacac aagagtgcac ccggtctcag 1080  
 taatattgtc tcggataaga aagaagggtg gcagtatatg ccatgcaaaa caggtgcgtg 1140  
 tgggtgttct ccaagtggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt 1200  
 gccatgcctg gtcaaaaggaa cttgttccag gctcagtgca cctcaacacc ccgctcgcgc 1260

aaattgagca gtgggcatcc ggctgtacag taagatcggc ctgggggggc gtgttccgaa 1320  
 gtaaaaaggt ggtgggttgc ttacggacaa ccttgatatc cacttgata ttttcaccac 1340  
 ctcttccgc ccgagaagcaa gcattgggtg aaaaatccat cctgggctac tatagcaaga 1440  
 tagtcttcgt atgggacaag cctgggtggc gcgaacaagg cttctcgggc gtctccaat 1500  
 ccagctgtga ccccatctca ttgccaagag ataccagcat cgaagtccat cggcaatggc 1560  
 ccattacctg tttcatggtc ggagaccggc gacggaagtg gtcccaacag tccaaagcag 1620  
 taogacagaa gtctgtctgg aaccaactcc ggcgagccta ccgagaacgac ggggcaccaag 1680  
 tccagagccc ggccaacgtg ctgagatcgc agtggctcgaa gcagcagtat tcccaaggag 1740  
 cgcagagccc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctccagaacgc 1800  
 cgttcaaggc tgttcatttc gttggaacgc agacgtcttt ggtttggaaa gggatatgg 1860  
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 cagcatag 1928

<210> 44  
 <211> 501  
 <212> PRT  
 <213> Rhinocycladiella atrovirens

<400> 44

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro  
 1 5 10 15

Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val  
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
 65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
 115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn  
 180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys  
 195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
 210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr  
 225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu  
 245 250 255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala  
 260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
 275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg  
 290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr  
 305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys

325

330

335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu  
 340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn  
 355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg  
 370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr  
 385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 405 410 415

Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 435 440 445

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu  
 450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
 465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
 530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
 545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 565 570 575

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 580 585 590

+0210 45  
 +0211 1928  
 +0212 DNA  
 +0213 Rhinocladiella atrovirens

+0220  
 +0221 Intron  
 +0222 (739)..(811)  
 +0223

+0224  
 +0225 Intron  
 +0226 (1184)..(1185)  
 +0227

+0400 45  
 atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc aggttatccc 60  
 cacgtcggcg taggccc aaa cggaggagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgcttcgg ccgtgacaga ccttgctac gagaaacagg ttgcccaagc attcgccaac 180  
 ctgcgagcct gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
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 gttgcggacg ttgtcgttgt gggcgttggc ttgagcgggt tggagacggc acgcaaagtc 480  
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 aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660  
 ctccagagga cgaacggaaa ttcaatccat caagcacaag acggtacaac cactacagt 720  
 ccttatgggt attccttgt aggcacaatt ccattctgtg atgagacctc tgtcgttgt 780  
 agaatacagt cgtgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc 840  
 ggaactcctt cccgcatggt ctacgtgat cgaagagcat agtcttgaag accccaaggc 900  
 gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

aaacttgoot gotgtttctcg gogtggcaaa ccagatcaca cgcgtctctgc tgggtgtgga 1020  
 agccacagag atcagcatgc tttttctcac cgaactacac aagagtggca cgggtctcag 1030  
 taatattgto tgggataaga aagacgggtgg gcagtatatg cgtatggcaaaa caggtgogtg 1140  
 tgggtgttctc tcagtgggag actcgtttct tagtggtoat tccaggtatg cagtcgtttt 1150  
 gccatgccat gtcaaaggaa cttgttccag gtcacgtgca cctcaacacc ccgtgcgcg 1160  
 aaattgajca gtgggcatcc ggctgtacag tacgacggc ctgggggggc gtgttcagaa 1170  
 gtaaaaaggt ggtgggtctcg ttacggacaa ccttgtatcc cactttgata ttttcaccac 1180  
 ctcttccgcg cgagaagcaa gcattgggtg aaaaatccat cctgggctac tatagcaaga 1190  
 tagtcttctt atgggacaag ctgtgggtgg gcgaacaagg cttctcgggc gtctccaat 1200  
 cgagctgtga ccccatctca tttgcacag ataccagcat cgaagtccat cggcaatggt 1210  
 ccattacctg tttcatggtc ggagacccgg gaagggaagt gtcccaacag tccaagcagg 1220  
 tacgacagaa gtctgtctgg aacccaactc ggcagacctc cagagaacgc ggggccccag 1230  
 tccagagcc ggccaacgtg ctccagatcg agtggctcga gcagcagtat ttccaaggag 1240  
 cgcagagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctccagaacgc 1250  
 cgttcaaggg tgttcatttc gttggaaagg agacgtcttt ggtttggaaa gggatatgg 1260  
 aaggggccat acgacgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1270  
 cagcatag 1280

<210> 46  
 <211> 591  
 <212> PRT  
 <213> *Rhinocycladiella atrovirens*

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala  
 1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr  
 20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala  
 35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu  
 50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr  
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu  
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro  
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr  
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe  
195 200 205

Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro  
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
245 250 255

Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp  
260 265 270

Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala  
275 280 285



His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
290 295 300

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
305 310 315 320

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
325 330 335

Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
340 345 350

Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
355 360 365

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
370 375 380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys  
385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu  
405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser  
420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser  
435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr  
450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp  
465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val  
485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro  
500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe  
515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala  
580 585 590

02100 47  
02110 600  
02120 PRT  
02130 Exophiala spinifera

04000 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
 225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
 260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
 275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
 325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<210> 48  
 <211> 1392  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cys 461 (Exophiala spinifera)

<220>  
 <221> CDS  
 <222> (1)..(1392)  
 <223>

<400> 48  
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15  
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc 144  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
 ggt ccc gcc agg acg act atc aac gac ctc gcc gct gcg tgg atc aat 192  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
 gag gcc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95  
 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110  
 gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125  
 atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140

egg ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac	430
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	503
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Gln Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gag aag aaa gac ggc	644
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	740
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370 375 380

cag gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa 1200  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

gga gct cag agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1243  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415

tcg gag ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt 1344  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

<210> 49  
 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteine 461 (Exophiala spinifera)

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
 165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
 180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
 195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
 210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
 225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
 245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
 260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 305 310 315 320



Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
 325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
 340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

<210> 50  
 <211> 1392  
 <212> DNA  
 <213> Unknown

<210>  
 <223> Cys (-) APAO; removal of cys 359 and 461 (Exophiala spinifera)

<220>  
 <221> CDS  
 <222> (1)..(1392)  
 <223>

<400> 50  
 aaa gac aac gtt gag gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15

ttg gag acg gca cgc aaa gtc bag gcc gcc ggt ctg tcc tgc ctc gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

20	25	30	
ctt gag ggc atg gat cgt gta ggg gga aag act ctg agc gta caa tgc Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45			144
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gag tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80			240
gag ggc gag ctg cag agg acg act gga aat tca ctc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt ggc gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag ggc aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tgc gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tgc att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tgc gca tcc ggc tgt aca gta cga tgc gcc tgc Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ctg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Gln Lys Gln	
275 280 285	
aaa ttg ggc gaa aat tct atc ctc ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Ala Gln Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
cta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tgc gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Gln Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tgc agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tct ttc atc gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cug aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc ccc gca gcc tac gag aac gcc ggc gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Gln Asn Ala Gly Ala Gln Val Pro Gln	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Gln Ile Gln Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tgc gcc ctc aga aac ccg ttc aag agt gtt cat ttc gtt gga aac gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Gln	
420 425 430	
aac tct tta gtt tgg aaa ggc tat atg gaa ggc gcc ata cga tgc ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Gln Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Gln Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	

<210> 51  
 <211> 463  
 <212> PRT

0213> Unknown

0220>

0223> Cys (-) APAO; removal of cys 359 and 461 (Exophiala spinifera)

0400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

1210 - 52  
 1211 - 1392  
 1212 - DNA  
 1213 - Unknown

1220 -  
 1223 - Cys (-) APAO; removal of cys 169, 359, and 461 (*Exophiala spinifera*)

1230 -  
 1231 - CDS  
 1232 - (1)..(1392)  
 1233 -

1400 - 52  
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc ggt ggc ttg agc ggt 43  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15  
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
 20 25 30  
 ctt gag acg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg 144  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
 ggt ccc ggc agg acg act atc aac gac ctc ggc ggt ggc tgg atc aat 192  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95  
 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110  
 gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125  
 atc gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag ggc aag 432  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys

130	135	140	
egg ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			523
ggt gtg gaa ggc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gct acc ggt ctc aat aat att ttc tog gac aag aac gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			634
ggg cag tat atg cga tgc aca aca ggt atg cag tog att tog cat ggc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tog gca tcc ggc tgt aca gta cga tog ggc tog Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768
ggc gcc gtg ttc cga agc aca aag gtg gtg gtt tog tta ccc aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270			816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285			864
gca ttg ggc gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300			912
gta tgg gac aag ccc tgg tgg cgc gaa caa ggc ttc tog gcc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320			960
caa tog agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335			1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccc gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350			1056
egg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365			1104

gac caa ctc cgg gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370 375 380

cgg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa 1200  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

gga gct cgg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1240  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415

tgg cgg ctc aga acg cgg ttc aag agt gtt cat ttc gtt gga acg gag 1296  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

acg gct tta gtc tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt 1344  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
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 450 455 460

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 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cys 169, 359, and 461 (Exophiala spinifera)

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
 20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln



Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460